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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 07:51:23 ; Search time 202.3 Seconds
(without alignments)
4729.486 Million cell updates/sec

Title: US-09-602-833a-1
Perfect score: 1116
Sequence: 1 atggacataaagtgtgtgtt.....ctttagccttcaatttga 1116

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_1101:*

1: /SID2/gcgdata/geneseq/geneseq/NA1980.DAT:*

2: /SID2/gcgdata/geneseq/geneseq/NA1981.DAT:*

3: /SID2/gcgdata/geneseq/geneseq/NA1982.DAT:*

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19: /SID2/gcgdata/geneseq/geneseq/NA1998.DAT:*

20: /SID2/gcgdata/geneseq/geneseq/NA1999.DAT:*

21: /SID2/gcgdata/geneseq/geneseq/NA2000.DAT:*

22: /SID2/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1116	AAF24902	Nucleotide sequence
2	681	61.0	681	AAF24903	Nucleotide sequence
3	130.4	11.7	2056	AAH17218	Human cDNA sequence
4	92.8	8.3	936	AAF58252	Oligonucleotide D1
5	92.8	8.3	936	AAF58254	Oligonucleotide D1
6	92.8	8.3	936	AAF58257	Oligonucleotide D1
7	92.8	8.3	936	AAF58259	Oligonucleotide D2
8	92.8	8.3	936	AAF58262	Oligonucleotide D2
9	92.8	8.3	936	AAF58255	Oligonucleotide D1
10	92.6	8.3	936	AAF58252	Oligonucleotide D1
11	92.6	8.3	936	AAF58254	Oligonucleotide D1

12	92.6	8.3	936	AAF58257	Oligonucleotide D1
13	92.6	8.3	936	AAF58259	Oligonucleotide D2
14	92.6	8.3	936	AAF58262	Oligonucleotide D2
15	92.6	8.3	938	AAF58255	Oligonucleotide D1
16	63.2	5.7	2840	AAH24250	Human Ras-binding
17	63.2	5.7	2847	AAH17735	Human cDNA sequence
18	57.4	5.1	1600	AA161075	Human polynucleoti
19	57.4	5.1	1947	AAH52247	Protein PRO239 cDN
20	57.4	5.1	1947	AAH72405	Human PRO239 cDNA
21	57.4	5.1	2384	AAH30919	Human secreted pro
22	57.4	5.1	2384	AAH83398	Human cDNA clone A
23	57.4	5.1	2412	AA159289	Human polynucleoti
24	57.4	5.1	2641	AA529427	HTM clone 2709055
25	56.8	5.1	6242	AAH99495	Human cDNA encodin
26	55.8	5.0	2410	AAH14179	Human cDNA sequenc
27	55.8	5.0	5199	AA158154	Human polynucleoti
28	55.2	4.9	3159	AAH99494	Human DNA encoding
29	55.2	4.9	3400	AAH72745	Human ORFX ORF2153
30	55.2	4.9	6125	AAH72745	Human cervical can
31	53.2	4.8	2620	AAH14529	Human cDNA sequenc
32	52.6	4.7	3138	AAH30202	Human RING finger
33	51.8	4.6	495	AAH26184	CDNA encoding mult
34	51.8	4.6	495	AAH26184	Skin cell cDNA, SE
35	51.8	4.6	2169	AAH30203	Human RING finger
36	51	4.6	1986	AAH26548	DNA encoding human
37	51	4.6	6470	AAH158376	Human polynucleoti
38	50.4	4.5	2527	AAH15457	Human cDNA sequenc
39	49.8	4.5	2694	AAH245671	Nucleotide sequenc
40	49	4.4	502	AAH00229	Human secreted pro
41	49	4.4	3938	AAH03265	Murine p53-induced
42	48.8	4.4	1710	AAH33095	Human colon cancer
43	48	4.3	528	AAH06111	Human cDNA clone (
44	46.8	4.2	3205	AAH34518	Death activator de
45	46.2	4.1	861	AAH06813	Human cDNA clone (

ALIGNMENTS

RESULT 1	
AAF24902	AAF24902 standard; cDNA; 1116 BP.
XX	XX
AC	AAF24902:
XX	XX
DT	20-APR-2001 (first entry)
XX	XX
DE	Nucleotide sequence of a human SGT4.1 polypeptide.
XX	XX
KW	Human: SGT4; signal transduction; guanosine triphosphate binding protein;
KW	GTP binding protein; cancer; immune response; nutritional source;
KW	animal feed; ss.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..1116
FT	/*tag= a
FT	/product= "SGT4"
PN	WO200078959-A1.
XX	XX
PD	28-DEC-2000.
XX	XX
PF	22-JUN-2000; 2000WO-US17248.
XX	XX
PR	23-JUN-1999; 99US-0140627.
XX	XX
PA	(LEXI-) LEXICON GENETICS INC.
XX	XX
PI	Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;
XX	XX
DR	WPI; 2001-032329/04.

DR P-PSDB: AAB31563.

XX New SGT4 genes and proteins, useful for diagnosing and treating
PT disorders involving inappropriate regulation of a signal transduction
PT mechanism e.g. cancer -

XX Claim 1; Fig 1; 82pp; English.

XX The present sequence encodes a human SGT4 polypeptide. SGT4 polypeptides
CC are involved in signal transduction pathways regulated by guanosine
CC triphosphate (GTP) binding proteins). SGT4 polynucleotides and
CC polypeptides are for diagnosing and treating conditions related to a
CC signal transduction mechanism involving SGT4 such as cancer. In
CC addition, it can be used to detect the expression of SGT4 as markers of
CC specific cells and tissues such as neuronal tissue, heart, liver,
CC pancreas and adrenal gland. They are also useful for the construction of
CC transgenic and knockout animals for studying SGT4 function in vivo and
CC for the screening of SGT4 (ant)agonists in an animal model. Other more
CC general uses include: as molecular weight markers on Southern gels; as
CC chromosome markers or tags; as probes; for selecting and making
CC oligomers for attachment to a gene chip; to raise anti-protein or
CC anti-DNA antibodies or to elicit immune response. They are also
CC also be used as nutritional sources or supplements such as in animal
CC feed.

XX Sequence 1116 BP; 343 A; 224 C; 265 G; 284 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;

Best Local Similarity 100.0%; Pred. NO. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggagacataaagtgtgtcttgcacattctgtcatcagaagccttgttggaactcgt 60
Db 1 atggagacataaagtgtgtcttgcacattctgtcatcagaagccttgttggaactcgt 60

QY 61 gtcaagaagcacaaagcttgcagagaagaagtgtaaaagcttgagaagcgcttg 120
Db 61 gtcaagaagcacaaagcttgcagagaagaagtgtaaaagcttgagaagcgcttg 120

QY 121 gagaagataaagaagagtggaacttctgtgcgaatcagaagagaaggaaccccccag 180
Db 121 gagaagataaagaagagtggaacttctgtgcgaatcagaagagaaggaaccccccag 180

QY 181 gctgtatactgcaagaatgtgtcttcatagaccacagctgtgcgctcttgacaagttaa 240
Db 181 gctgtatactgcaagaatgtgtcttcatagaccacagctgtgcgctcttgacaagttaa 240

QY 241 aggaacactctacaaagcagaagcttcccaagagacagagcaaacgagcgactgcg 300
Db 241 aggaacactctacaaagcagaagcttcccaagagacagagcaaacgagcgactgcg 300

QY 301 ttgtgttctgaacttctcgggagacacgtgagagctcccccagatttgaagagcag 360
Db 301 ttgtgttctgaacttctcgggagacacgtgagagctcccccagatttgaagagcag 360

QY 361 acacacctgagaagatggtacaaatcattgattcaaatcattcctacatatt 420
Db 361 acacacctgagaagatggtacaaatcattgattcaaatcattcctacatatt 420

QY 421 cagttatttcaagcagatagaaattctgattcgcacaaaacaaatcccatcttcca 480
Db 421 cagttatttcaagcagatagaaattctgattcgcacaaaacaaatcccatcttcca 480

QY 481 gcagaacatcggtgtgttgaagaacctgaaagacatctgtgttcaactatgag 540
Db 481 gcagaacatcggtgtgttgaagaacctgaaagacatctgtgttcaactatgag 540

QY 541 agcatctctcagaattggagatgtgaaaaactagagagagctgattgttctgaaat 600
Db 541 agcatctctcagaattggagatgtgaaaaactagagagagctgattgttctgaaat 600

QY 601 ctagaattaatgagagctcccttgaattaagtaattggaagcaagttacattttagat 660
Db 601 ctagaattaatgagagctcccttgaattaagtaattggaagcaagttacattttagat 660

Db 601 ctagaattaatgagagctcccttgaattaagtaattggaagcaagttacattttagat 660

QY 661 atctcagaacaaatttcccaagtgctcccaatctgtcccgaggatctgaattgcag 720

Db 661 atctcagaacaaatttcccaagtgctcccaatctgtcccgaggatctgaattgcag 720

QY 721 tgttggatatacgaagaataaaccctgacgacctgcgcgaagatagagaagctagag 780

Db 721 tgttggatatacgaagaataaaccctgacgacctgcgcgaagatagagaagctagag 780

QY 781 gagctgcagagcttctctgtataaacaagttgaccttaccttccattcctatctg 840

Db 781 gagctgcagagcttctctgtataaacaagttgaccttaccttccattcctatctg 840

QY 841 aacctgagaagagctacctctttagctgtcagctgtggagacatttggtagctcccaact 900

Db 841 aacctgagaagagctacctctttagctgtcagctgtggagacatttggtagctcccaact 900

QY 901 gcccttctgtactatccacacctttaaatttgtaagccttatggaacatcctatgat 960

Db 901 gcccttctgtactatccacacctttaaatttgtaagccttatggaacatcctatgat 960

QY 961 aatgcccgaatgtgaagatgagcaatgaaataatggaagtgaaacgagatccgcaacattt 1020

Db 961 aatgcccgaatgtgaagatgagcaatgaaataatggaagtgaaacgagatccgcaacattt 1020

QY 1021 gataaagaagtataaagcctatataatgaagacctaagaagaagaaatctgttccagc 1080

Db 1021 gataaagaagtataaagcctatataatgaagacctaagaagaagaaatctgttccagc 1080

QY 1081 tataccacaaagtgctctttagccttcaacttga 1116

Db 1081 tataccacaaagtgctctttagccttcaacttga 1116

RESULT 2

AAE24903

ID AAE24903 standard; cDNA: 681 BP.

AAE24903;

20-APR-2001 (first entry)

Nucleotide sequence of a human SGT4-2 polypeptide.

Human; SGT4; signal transduction; guanosine triphosphate binding protein;
KW GTP binding protein; cancer; immune response; nutritional source;
KW animal feed; ss.

OS Homo sapiens.

Key Location/Qualifiers
FH 1..681
FT CDS /tag= a
FT /product= "SGT4"

WO200078959-A1;

28-DEC-2000.

22-JUN-2000; 2000WO-US17248.

23-JUN-1999; 99US-0140627.

(LEXI-) LEXICON GENETICS INC.

Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;
WPI; 2001-032329/04.
P-PSDB: AAB31564.

New SGT4 genes and proteins, useful for diagnosing and treating

[illegible]

OY	439	agaatttgatctgcgaataaaaccaaactcaactcattccagcaatctgattgttg	498
Db	668	ww	629
OY	499	aagaacctgaagaactcaactgtg99lttcaactactgtgaagacattcctccagaattg	558
Db	628	ww	569
OY	559	ggagattgtgaaaactctagagagactcgtgattgttcttggaactctgaatttaagagctg	618
Db	568	ww	509
OY	619	cccttgaattgaatgaatttgaagcaagttacattgtgatatactcaagaacaagt	678
Db	508	ww	449
OY	679	tccagtgctccaaactctgtctcctcgagatcgaaatttcagtggttgatacaagcagc	738
Db	448	ww	389
OY	739	aataactgacgcagctctgcgcgaagatagacagcctagagagctcagaactctctc	798
Db	388	ww	329
OY	799	tgtgataaaacaagtgtagactcattccctacttccatctgactgaacctgaagaagctact	858
Db	328	ww	269
OY	859	ctgttagctgcagtg99ggaccaatttgtgtgagctcccaactgccttltgactcacc	918
Db	268	ww	209
OY	919	acacctttaaatttgtaagccttatgacaaactctatgtataatgcccgaatggaagt	978
Db	208	ww	149
OY	979	ggcaatgaataatggaagaatggaagcgagatcgccacatttggataaagaattatgaa	1038
Db	148	ww	89
OY	1039	gctcatactgaagaccttaagaagaagaatctgttccagctataccacaagaatgtct	1098
Db	88	ww	29
OY	1099	tttagccttcaactt 1114	
Db	28	wwwwwwwwwwwwwwwwww 13	
RESULT 5			
AAFS8254/c			
ID	AAFS8254 standard; DNA; 936 BP.		
XX			
NC	AAFS8254;		
XX			
DT	24-APR-2001 (first entry)		
XX			
DE	Oligonucleotide D1875.		
XX			
KM	Electron-transfer group; ETW; mismatch; genotyping;		
KW	gene expression; ss.		
XX			
OS	Synthetic.		
XX			
PN	WO200107665-A2.		
XX			
PD	01-FEB-2001.		
XX			
PF	26-JUL-2000; 2000MO-US20476.		
XX			
PR	26-JUL-1999; 99US-0145695.		
PR	17-MAR-2000; 2000US-0190259.		
XX			

[illegible]

XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX
SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match	8.38;	Score 92.8;	DB 22;	Length 936;
Best Local Similarity	2.0%;	Pred. No. 5,2e-18;		
Matches	16;	Conservative 454;	Mismatches 326;	Indels 0;
			Gaps	0;

[illegible]

[illegible]

AA58257	RESULT 12
ID	AAF58257 standard; DNA; 936 BP.
XX	
AC	AAF58257;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D1954.
XX	
KW	Electron-transfer group; ETW; mismatch; genotyping; gene expression; ss.

OS Synthetic.
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
PI
XX WPI: 2001-159728/16.
DR
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CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 8.3%; Score 92.6; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 6e-18;
Matches 5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;

QY 374 aatggtacataagcaactctgattcaatcctcctcatatattcagttcaag 433
DB 10 www.
QY 434 cgatgagaattctgcatctgcacaaaacacatctcacatcttcacagagaatcggtt 493
DB 70 www.
QY 494 gtttgaagaacctgaagaactcaatgtggttcaactatctgaagagactcctccag 553
DB 130 www.
QY 554 aattggagattgtgaataatctagagagactgattgttcttgtaaatctagaattatgg 613
DB 190 www.
QY 614 agctgccttgaacttaatttgaagcaagttacattctgttagatctcagcaanaa 673
DB 250 www.
QY 674 agtttccagtgcccaactctgttcctcgtgagatgtcgaattgagtggtgatata 733
DB 310 www.
QY 734 gcagcaataactgcagcagctgcgcgaagatagacagcgttagagagctgcagact 793
DB 370 www.
QY 794 tctcttgatataaaaagaattgacctactcctcattcactgctgaacctggaagac 853
DB 430 www.
QY 854 tcaactgttaagtcgacgagtggaacattgttgagagctcccaactgccttctgact 913
DB 490 www.

QY 914 catcacaccttaaaattgtgaagccttatgagacaatcctcttgaataatgcccaatgtg 973
DB 550 www.
QY 974 aagatggcaatgaataatgaaatgaaagtgacgggactgcacacatttgaataagaatga 1033
DB 610 www.
QY 1034 tgaagcctataatgaagacctaaagaagaatctgttccagctataccaccaag 1093
DB 670 www.
QY 1094 tgcctttagccttcaactt 1114
DB 730 www.

RESULT 13
AAF58259
ID AAF58259 standard; DNA; 936 BP.
XX
XX AAF58259;
AC
XX
XX 24-APR-2001 (first entry)
DT
XX
XX Oligonucleotide D2004.
DE
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
KW
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX
XX 01-FEB-2001.
PD
XX
XX 26-JUL-2000; 2000WO-US20476.
PF
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX
XX Umek RM;
PI
XX
XX WPI: 2001-159728/16.
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CC detection of nucleic acids, especially of substitutions (mismatches)
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XX
XX Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
SQ

Query Match 8.3%; Score 92.6; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 6e-18;
Matches 5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;

QY 374 aatggtacataagcaactctgattcaatcctcctcatatattcagttcaag 433
DB 10 www.
QY 434 cgatgagaattctgcatctgcacaaaacacatctcacatcttcacagagaatcggtt 493
DB 490 www.

Db 70 www..... 129
QY 494 gtttgaagaacctgaagaactgaatgtgggttccaatctcgaagagcttccctcag 553
Db 130 www..... 189
QY 554 aattggagattgtgaatactagagagactgattctcgaatactgaataatg 613
Db 190 www..... 249
QY 614 agctgaccttgaataaattgaagaagttacattttagatactcagaaca 673
Db 250 www..... 309
QY 674 agtttccagtgcacctgtgtcctgcgagatgcgaatttgcaatgtttagata 733
Db 310 www..... 369
QY 734 gcagcaataacctgacacctgcgcgaagatagacagctagagagctgagagct 793
Db 370 www..... 429
QY 794 ttctctgtataaacaagttgacctacttccctatccatgctgaacctgaagaagc 853
Db 430 www..... 489
QY 854 tcaactcgttagtcgtgaatggtgagacatttgtgtgagctcccaactgcttgaact 913
Db 490 www..... 549
QY 914 catccacaccttgaataattgtgaagctttagacaatcctattgataatgccaatgtg 973
Db 550 www..... 609
QY 974 aagatgcaatgaataatggaagtgacggagctgcgaacattttagataaagaagta 1033
Db 610 www..... 669
QY 1034 tgaagcctatatgaagaccttaagaagaagatctgttccagctataccccaag 1093
Db 670 www..... 729
QY 1094 tgtctttagacctcaactt 1114
Db 730 www..... 750

RESULT 14
AAF58262
ID AAF58262 standard; DNA; 936 BP.
XX
AC AAF58262;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2007.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; SS.
XX
OS Synthetic.
XX
PN MO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX

PI Uniek RM;
XX
DR WPI; 2001-159728/16.
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PT Nucleic acids containing electron-transfer group, useful as labels in
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CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 8 3%; Score 92.6; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 6e-18; 295; Indels 0; Gaps 0;
Matches 5; Conservative 44; Mismatches 295; Indels 0; Gaps 0;

QY 374 aatggtacataagcaataacctgtgattcaatcattccatataatcaatttcaag 433
Db 10 www..... 69
QY 434 cgaatgaatcttgatctgcgaataacccaatccatccatccagcagaatcggt 493
Db 70 www..... 129
QY 494 gtttgaagaacctgaagaactgaatgtgggttccaatctcgaagagcttccctcag 553
Db 130 www..... 189
QY 554 aattggagattgtgaatactagagagactgattctcgaatactgaataatg 613
Db 190 www..... 249
QY 614 agctgaccttgaataaattgaagaagttacattttagatactcagaaca 673
Db 250 www..... 309
QY 674 agtttccagtgcacctgtgtcctgcgagatgcgaatttgcaatgtttagata 733
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QY 734 gcagcaataacctgacacctgcgcgaagatagacagctagagagctgagagct 793
Db 370 www..... 429
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Db 430 www..... 489
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QY 1094 tgtctttagacctcaactt 1114

